IN THE CLAIMS

1-59. (canceled)

60. (currently amended) A hypermutable transgenic mouse wherein ~~at least 50% of the~~ cells of said mouse comprise a dominant negative allele of a *PMS2* mismatch repair gene, wherein said dominant negative allele comprises a truncation mutation.

61. (currently amended) A hypermutable, transgenic mouse produced by a process comprising the steps of:

introducing a polynucleotide comprising a sequence encoding a dominant negative allele of a *PMS2* mismatch repair gene into a fertilized mouse egg, wherein the dominant negative allele comprises a truncation mutation, whereby said fertilized mouse egg becomes hypermutable;

implanting the fertilized egg into a pseudopregnant female; and

allowing said mouse egg to develop into a hypermutable, transgenic mouse.

62. (previously presented) A method of making a hypermutable, fertilized mouse egg comprising introducing into said fertilized mouse egg a polynucleotide comprising a sequence encoding a dominant negative allele of a *PMS2* mismatch repair gene, wherein the dominant negative allele comprises a truncation mutation, whereby said fertilized mouse egg becomes hypermutable.

63-70. (canceled)

71. (currently amended) A method for generating a mutation in a gene of interest comprising the steps of:

introducing a polynucleotide comprising a dominant negative allele of a *PMS2* mismatch repair gene into a fertilized mouse egg, wherein the dominant negative allele comprises a truncation mutation, whereby the fertilized mouse egg becomes hypermutable;

implanting the fertilized egg into a pseudopregnant female;

allowing said fertilized mouse egg to develop into a hypermutable, transgenic mouse; and

testing the mouse to determine whether the gene of interest harbors a mutation.

72. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing a nucleotide sequence of the gene of interest.

73. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing mRNA transcribed from the gene of interest.

74. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing a protein encoded by the gene of interest.

75. (previously presented) The method of claim 71 wherein the step of testing comprises analyzing the phenotype of the gene of interest.

76-80. (canceled)

81. (previously presented) The method of claim 62 wherein the mismatch repair gene is human *PMS2*.

82. (previously presented) The method of claim 81 wherein said mismatch repair gene comprises a truncation mutation at codon 134 as shown in SEQ ID NO:1.

83. (previously presented) The method of claim 82 wherein the truncation mutation is a thymidine at nucleotide 424 of wild-type *PMS2* as shown in SEQ ID NO:1.

84. (previously presented) The hypermutable, transgenic mouse of claim 60 comprising a protein which consists of the first 133 amino acids of human PMS2.

85. (previously presented) The hypermutable, transgenic mouse of claim 61 wherein the mismatch repair gene is human *PMS2*.

86. (previously presented) The hypermutable, transgenic mouse of claim 61 wherein the dominant negative allele comprises a truncation mutation at codon 134 as shown in SEQ ID NO:1.

87. (previously presented) The hypermutable, transgenic mouse of claim 86 wherein the truncation mutation is a thymidine at nucleotide 424 of wild-type *PMS2* as shown in SEQ ID NO:1.